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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/838,785

DATE: 05/08/2001
TIME: 15:43:16

Input Set : A:\A-0341.app
Output Set: N:\CRF3\05082001\I838785.raw

ENTERED

3 <110> APPLICANT: Lau, Ted
4 Lin, Rick
5 Parkes, Debbie
6 Parry, Gordon
7 Schneider, Douglas
8 Steinbrecher, Renate
9 Van Heuit, Pam T
10 Wu, John
12 <120> TITLE OF INVENTION: DNA Encoding a Novel PROST 03
14 <130> FILE REFERENCE: 51831AUSM1
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/838,785
C--> 17 <141> CURRENT FILING DATE: 2001-04-20
19 <150> PRIOR APPLICATION NUMBER: 60/200,065
20 <151> PRIOR FILING DATE: 2000-04-27
22 <160> NUMBER OF SEQ ID NOS: 26
24 <170> SOFTWARE: PatentIn Ver. 2.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 3320
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (282)..(1943)
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40 gctggaccgg caccaaaggg ctggcagaaa tgggcgcctg gctgattcct aggcagtttg 180
42 cggcagcaag gaggagaggc cgcagcttct ggagcagagc cgagacgaag cagttctgga 240
44 gtgcctgaac ggccccctga gccctaccgc cctggcccac t atg gtc cag agg ctg 296
45 Met Val Gln Arg Leu
46 1 5
48 tgg gtg agc cgc ctg ctg cgg cac cgg aaa gcc cag ctc ttg ctg gtc 344
49 Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu Leu Leu Val
50 10 15 20
52 aac ctg cta acc ttt ggc ctg gag gtg tgt ttg gcc gca ggc atc acc 392
53 Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu Ala Ala Gly Ile Thr
54 25 30 35
56 tat gtg ccg cct ctg ctg ctg gaa gtg ggg gta gag gag aag ttc atg 440
57 Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met
58 40 45 50
60 acc atg gtg ctg ggc att ggt cca gtg ctg ggc ctg gtc tgt gtc ccg 488
61 Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
62 55 60 65
64 ctc cta ggc tca gcc agt gac cac tgg cgt gga cgc tat ggc cgc cgc 536
65 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
66 70 75 80 85
68 cgg ccc ttc atc tgg gca ctg tcc ttg ggc atc ctg ctg agc ctc ttt 584

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69 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
70          90          95          100
72 ctc atc cca agg gcc ggc tgg cta gca ggg ctg ctg tgc ccg gat ccc 632
73 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
74          105          110          115
76 agg ccc ctg gag ctg gca ctg ctc atc ctg ggc gtg ggg ctg ctg gac 680
77 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
78          120          125          130
80 ttc tgt ggc cag gtg tgc ttc act cca ctg gag gcc ctg ctc tct gac 728
81 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
82          135          140          145
84 ctc ttc cgg gac ccg gac cac tgt cgc cag gcc tac tct gtc tat gcc 776
85 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
86 150          155          160          165
88 ttc atg atc agt ctt ggg ggc tgc ctg ggc tac ctc ctg cct gcc att 824
89 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
90          170          175          180
92 gac tgg gac acc agt gcc ctg gcc ccc tac ctg ggc acc cag gag gag 872
93 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
94          185          190          195
96 tgc ctc ttt ggc ctg ctc acc ctc atc ttc ctc acc tgc gta gca gcc 920
97 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
98          200          205          210
100 aca ctg ctg gtg gct gag gag gca gcg ctg ggc ccc acc gag cca gca 968
101 Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
102          215          220          225
104 gaa ggg ctg tcg gcc ccc tcc ttg tcg ccc cac tgc tgt cca tgc cgg 1016
105 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
106 230          235          240          245
108 gcc cgc ttg gct ttc cgg aac ctg ggc gcc ctg ctt ccc cgg ctg cac 1064
109 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
110          250          255          260
112 cag ctg tgc tgc cgc atg ccc cgc acc ctg cgc cgg ctc ttc gtg gct 1112
113 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
114          265          270          275
116 gag ctg tgc agc tgg atg gca ctc atg acc ttc acg ctg ttt tac acg 1160
117 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
118          280          285          290
120 gat ttc gtg ggc gag ggg ctg tac cag ggc gtg ccc aga gct gag ccg 1208
121 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
122          295          300          305
124 ggc acc gag gcc cgg aga cac tat gat gaa ggc gtt cgg atg ggc agc 1256
125 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
126 310          315          320          325
128 ctg ggg ctg ttc ctg cag tgc gcc atc tcc ctg gtc ttc tct ctg gtc 1304
129 Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
130          330          335          340
132 atg gac cgg ctg gtg cag cga ttc ggc act cga gca gtc tat ttg gcc 1352
133 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala

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134          345          350          355
136 agt gtg gca gct ttc cct gtg gct gcc ggt gcc aca tgc ctg tcc cac 1400
137 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
138          360          365          370
140 agt gtg gcc gtg gtg aca gct tca gcc gcc ctc acc ggg ttc acc ttc 1448
141 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
142          375          380          385
144 tca gcc ctg cag atc ctg ccc tac aca ctg gcc tcc ctc tac cac cgg 1496
145 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
146 390          395          400          405
148 gag aag cag gtg ttc ctg ccc aaa tac cga ggg gac act gga ggt gct 1544
149 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
150          410          415          420
152 agc agt gag gac agc ctg atg acc agc ttc ctg cca ggc cct aag cct 1592
153 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
154          425          430          435
156 gga gct ccc ttc cct aat gga cac gtg ggt gct gga ggc agt ggc ctg 1640
157 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
158          440          445          450
160 ctc cca cct cca ccc gcg ctc tgc ggg gcc tct gcc tgt gat gtc tcc 1688
161 Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser
162          455          460          465
164 gta cgt gtg gtg gtg ggt gag ccc acc gag gcc agg gtg gtt ccg ggc 1736
165 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly
166 470          475          480          485
168 cgg ggc atc tgc ctg gac ctc gcc atc ctg gat agt gcc ttc ctg ctg 1784
169 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu
170          490          495          500
172 tcc cag gtg gcc cca tcc ctg ttt atg ggc tcc att gtc cag ctc agc 1832
173 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser
174          505          510          515
176 cag tct gtc act gcc tat atg gtg tct gcc gca ggc ctg ggt ctg gtc 1880
177 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
178          520          525          530
180 gcc att tac ttt gct aca cag gta gta ttt gac aag agc gac ttg gcc 1928
181 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala
182          535          540          545
184 aaa tac tca gcg tag aaaacttcca gcacattggg gtggagggcc tgcctcactg 1983
185 Lys Tyr Ser Ala
186 550
188 ggtcccgact ccccgctcct gttagcccca tggggetgcc gggctggccg ccagtttctg 2043
190 ttgctgccaa agtaatgtgg ctctctgtg ccacctgtg ctgtgaggt gcgtagctgc 2103
192 acagctgggg gctggggcgt cctctctctc tctccccagt ctctagggct gctgactgg 2163
194 aggccttcca agggggtttc agtctggact tatacaggga ggccagaagg gctccatgca 2223
196 ctggaatgcg gggactctgc aggtggatta cccaggctca gggttaacag ctagecctcct 2283
198 agttgagaca cacctagaga aggttttttg ggagctgaat aaactcagtc acctggtttc 2343
200 ccattctctaa gccccttaac ctgcagcttc gtttaatgta gctcttgcat gggagtttct 2403
202 aggatgaaac actcctccat gggatttgaa catatgaaag ttattttagt gggaagagtc 2463
204 ctgagggggca acacacaaga accaggtccc ctcagccac agcactgtct ttttctgat 2523

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206 ccacccccct cttacctttt atcaggatgt ggcctgttg tctttctgtt gccatcacag 2583
208 agacacaggc atttaaatat ttaacttatt tatttaacaa agtagaaggg aatccattgc 2643
210 tagcttttct gtgttggtgt ctaatatattt ggtagggtgg gggatcccca acaatcagggt 2703
212 cccctgagat agctgggtcat tgggctgac attgccagaa tcttcttctc ctgggggtctg 2763
214 gccccccaaa atgcctaacc caggacctg gaaattctac tcatcccaaa tgataattcc 2823
216 aaatgctgtt acccaagggt aggggtgtga aggaaggtag aggggtggggc ttcagggtctc 2883
218 aacggcttcc ctaaccaccc ctcttctctt ggcccagcct ggttccccc acttccactc 2943
220 cctctactc tctctaggac tgggctgatg aaggcactgc ccaaatttc ccctaccccc 3003
222 aactttcccc taccaccaac ttccccacc agctccacaa ccctgtttgg agctactgca 3063
224 ggaccagaag cacaaagtgc ggtttcccaa gcctttgtcc atctcagccc ccagagtata 3123
226 tctgtgcttg ggaatctca cacagaaact caggagcacc ccctgcctga gctaaggag 3183
228 gtcttatctc tcaggggggg gtttaagtgc cgtttgcaat aatgtcgtct tatttattta 3243
230 gcggggtgaa tattttatata tgtaagttag caatcagagt ataagttaa tggtgacaaa 3303
232 attaaaggct ttcttat                                     3320
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237 <212> TYPE: PRT
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245      20              25              30
247 Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
248      35              40              45
250 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
251      50              55              60
253 Leu Val Cys Val Pro Leu Gly Ser Ala Ser Asp His Trp Arg Gly
254      65              70              75              80
256 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
257      85              90              95
259 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
260      100             105             110
262 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
263      115             120             125
265 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
266      130             135             140
268 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
269      145             150             155             160
271 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
272      165             170             175
274 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
275      180             185             190
277 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
278      195             200             205
280 Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
281      210             215             220
283 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
284      225             230             235             240

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286 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
287          245          250          255
289 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
290          260          265          270
292 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
293          275          280          285
295 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
296          290          295          300
298 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
299 305          310          315          320
301 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
302          325          330          335
304 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
305          340          345          350
307 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
308          355          360          365
310 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
311          370          375          380
313 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
314 385          390          395          400
316 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
317          405          410          415
319 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
320          420          425          430
322 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
323          435          440          445
325 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
326          450          455          460
328 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
329 465          470          475          480
331 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
332          485          490          495
334 Ser Ala Phe Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
335          500          505          510
337 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
338          515          520          525
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341          530          535          540
343 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
344 545          550
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353 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
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VERIFICATION SUMMARY

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Input Set : A:\A-0341.app

Output Set: N:\CRF3\05082001\I838785.raw

L:16 M:270 C: Current Application Number differs, Replaced Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date